



## SEQUENCE LISTING

<110> YOSHIOKA, HIROFUMI

<120> GERM-RESPONSIVE PROMOTER

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<140> 10/537,094

<141> 2005-06-02

<150> JP 2002-351701

<151> 2002-12-03

<150> JP 2003-294409

<151> 2003-08-18

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<170> PatentIn Ver. 3.3

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 <213> Solanum tuberosum

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 <213> Solanum tuberosum

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 35 40 45  
 Val Ala Leu Ala Val Pro Leu Pro Leu Pro Pro Thr Ser Ala Pro Ser  
 50 55 60  
 Ser Ser Ser Ser Ser Ser Pro Leu Pro Thr Pro Leu His Phe  
 65 70 75 80

Ser Glu Leu Glu Arg Val Asn Arg Ile Gly Ser Gly Thr Gly Gly Thr  
 85 90 95

Val Tyr Lys Val Leu His Arg Pro Thr Gly Arg Leu Tyr Ala Leu Lys  
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Val Ile Tyr Gly Asn His Glu Asp Ser Val Arg Leu Gln Met Cys Arg  
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Glu Ile Glu Ile Leu Arg Asp Val Asp Asn Pro Asn Val Val Arg Cys  
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His Asp Met Phe Asp His Asn Gly Glu Ile Gln Val Leu Leu Glu Phe  
 145 150 155 160

Met Asp Lys Gly Ser Leu Glu Gly Ile His Ile Pro Leu Glu Gln Pro  
 165 170 175

Leu Ser Asp Leu Thr Arg Gln Val Leu Ser Gly Leu Tyr Tyr Leu His  
 180 185 190

Arg Arg Lys Ile Val His Arg Asp Ile Lys Pro Ser Asn Leu Leu Ile  
 195 200 205

Asn Ser Arg Arg Glu Val Lys Ile Ala Asp Phe Gly Val Ser Arg Val  
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Tyr Met Ser Pro Glu Arg Ile Asn Thr Asp Leu Asn His Gly Gln Tyr  
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Asp Gly Tyr Ala Gly Asp Ile Trp Ser Leu Gly Val Ser Ile Leu Glu  
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Phe Tyr Leu Gly Arg Phe Pro Phe Ser Val Gly Arg Gln Gly Asp Trp  
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Ala Ser Leu Met Cys Ala Ile Cys Met Ser Gln Pro Pro Glu Ala Pro  
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Pro Thr Ala Ser Arg Glu Phe Arg Glu Phe Ile Ala Cys Cys Leu Gln  
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Arg Asp Pro Ala Arg Arg Trp Thr Ala Ala Gln Leu Leu Arg His Pro  
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Phe Ile Thr Gln Asn Ser Pro Gly Thr His Thr Gly Pro Ala Thr Thr  
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Ser Ser Ser Ser Ser Ser  
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<211> 1125
<212> DNA
<213> Artificial Sequence

<220>
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<211> 374
<212> PRT
<213> Artificial Sequence

<220>
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      construct

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Arg Pro Arg Arg Arg Thr Asp Leu Thr Leu Pro Leu Pro Gln Arg Asp
      35           40           45

Val Ala Leu Ala Val Pro Leu Pro Pro Thr Ser Ala Pro Ser
      50           55           60

Ser Ser Ser Ser Ser Ser Pro Leu Pro Thr Pro Leu His Phe
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Ser Glu Leu Glu Arg Val Asn Arg Ile Gly Ser Gly Thr Gly Gly Thr
      85           90           95

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Val Tyr Lys Val Leu His Arg Pro Thr Gly Arg Leu Tyr Ala Leu Lys  
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 130 135 140  
 His Asp Met Phe Asp His Asn Gly Glu Ile Gln Val Leu Leu Glu Phe  
 145 150 155 160  
 Met Asp Lys Gly Ser Leu Glu Gly Ile His Ile Pro Leu Glu Gln Pro  
 165 170 175  
 Leu Ser Asp Leu Thr Arg Gln Val Leu Ser Gly Leu Tyr Tyr Leu His  
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 Arg Arg Lys Ile Val His Arg Asp Ile Lys Pro Ser Asn Leu Leu Ile  
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 Asn Ser Arg Arg Glu Val Lys Ile Ala Asp Phe Gly Val Ser Arg Val  
 210 215 220  
 Leu Ala Gln Asp Met Asp Pro Cys Asn Asp Ser Val Gly Thr Ile Ala  
 225 230 235 240  
 Tyr Met Ser Pro Glu Arg Ile Asn Thr Asp Leu Asn His Gly Gln Tyr  
 245 250 255  
 Asp Gly Tyr Ala Gly Asp Ile Trp Ser Leu Gly Val Ser Ile Leu Glu  
 260 265 270  
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 Ala Ser Leu Met Cys Ala Ile Cys Met Ser Gln Pro Pro Glu Ala Pro  
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<220>
<223> Description of Artificial Sequence: Synthetic
primer

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<223> Description of Artificial Sequence: Synthetic
primer

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primer

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<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<400> 14  
gaagtaattha aatttaataa ttatcaa 27

<210> 15  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<400> 15  
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<210> 16  
<211> 20  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<400> 16  
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<210> 17  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<400> 17  
aggacatgt tcgacctggtt 20

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<210> 18
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 18
tctccatgag tccttacatg                                20

<210> 19
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 19
catcccttaa aattataagt attc                                24

<210> 20
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 20
ataaatgata caaaataaaat taagg                                25

<210> 21
<211> 2231
<212> DNA
<213> Solanum tuberosum

<400> 21
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tcaaggatg tcttagcaac gacatcagggt gtctattgaa cttatacgaa gcttcacatg 660

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 agatgttgc acaaacacgaa cttagtgaag tatcaaggta tacagatgtg ttaagttgaa 960  
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<210> 22  
 <211> 1337  
 <212> DNA  
 <213> Solanum tuberosum

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 aaataaaacaa aaggagagac actttcttgc tcccttcgag gccatataatc ccattaaat 240  
 aaaaatataa aacaaaaaaa aagacagacg gtgcggcaag gaaagaaggc ggacgtcact 300  
 aacggcttaac ccttaactaca aataatgttgc ttttccaaaa acggaactat aaggaataaaa 360  
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 ttttttttttgc agttatattat ttttttttttgc aaaaataaaat ttttttttttgc 540  
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 aaggcttgcatttgc ccactataaa tactcaatatttgc ttttttttttgc atttttttttgc atttttttttgc 1260  
 accaacttgcatttgc aaatatttgc aatatttgc gtttttttttgc atttttttttgc atttttttttgc 1320  
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<210> 23
<211> 50
<212> DNA
<213> Solanum tuberosum

<400> 23
gtccgcccctt actattccca tccgatctct tgggaagcgg gggagaaaaat 50

<210> 24
<211> 1288
<212> DNA
<213> Solanum tuberosum

<400> 24
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tttcaagttt aagacggaaa caatagcatt ggatcaagac agacgcattt gaaggaagaa 120
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caagctaattt agacccgttt ccgaagaa 1288

<210> 25
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 25
cggaatttctt gtaatcctta ttttaggat 30

<210> 26
<211> 30
<212> DNA
<213> Artificial Sequence

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<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<400> 26  
cggaattcgt ccgcccttac tattcccatc 30

<210> 27  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<400> 27  
cggaattctt tataatagtg cactcatgct 30

<210> 28  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<400> 28  
cggaattcgc tatatttttt caagttgaag 30

<210> 29  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<400> 29  
cggaattcga cgccattgaa ggaagaaaaaa 30

<210> 30  
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<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

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<400> 30
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<210> 31
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<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 31
cggaattcaa caaaaaaaaaa gacagacggt 30

<210> 32
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<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 32
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<210> 33
<211> 30
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 33
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<210> 34
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 34
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<210> 35  
<211> 30  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Synthetic primer

<400> 35  
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<210> 36  
<211> 28  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Synthetic primer

<400> 36  
ttgggccccat gcgacacctt caaccacc 28

<210> 37  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic primer

<400> 37  
gactagtaca aaagagtgtg gaattac 27

<210> 38  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic primer

<400> 38  
gtcgacgaca cagccacgtc cgaggt 26

<210> 39  
<211> 26  
<212> DNA  
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 39
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<210> 40
<211> 5236
<212> DNA
<213> Solanum tuberosum

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<222> (4583)..(4876)

<220>
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<222> (246)
<223> a, c, g, t, unknown or other

<220>
<221> modified_base
<222> (278)
<223> a, c, g, t, unknown or other

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tctactttaa ttttttcaa cctaaaccaa cgtacaataa tgtgtaatga tactaattt 120
actcacataa tagcatggtg ctagaagagt cacttggaaag agtataactga agagtattaa 180

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aaaaattcaa attcgaattc ttgtaatcct tatttaggat tattgcgacc atcacttgc 360  
ggtccttac ttgactaaat atttgattaa acattaattt ttggtcagtg gatatacatg 420  
ccactcaatt ttaaataaaat tagtgatccc ttacgatctt aaaaaattg tattttgtg 480  
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 tca ttc tct ctc gac aat cag gtaattactt aattaattac taattaaatc 2789  
 Ser Phe Ser Leu Asp Asn Gln  
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 cttctctatc gcttatattt ggtaattac tactaatccc aatcatgaac attttacag 2848  
  
 gtt gct gaa aag tat gct caa gag att gaa act ttg aag gaa caa aca 2896  
 Val Ala Glu Lys Tyr Ala Gln Glu Ile Glu Thr Leu Lys Glu Gln Thr  
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 agg agt ttg ttg tct gct gct ttt ggt gtaata aca ttg gct gag aaa 2944  
 Arg Ser Leu Leu Ser Ala Ala Ala Cys Gly Ile Thr Leu Ala Glu Lys  
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 ttg aat ctg ata gac att gtt gag cgc ctt ggc tta gct tat cat ttt 2992  
 Leu Asn Leu Ile Asp Ile Val Glu Arg Leu Gly Leu Ala Tyr His Phe  
     70                75                80                85  
  
 gag aaa caa ata gat gat atg ttg gat caa att tac aaa gca gat ccc 3040  
 Glu Lys Gln Ile Asp Asp Met Leu Asp Gln Ile Tyr Lys Ala Asp Pro  
     90                95                100  
  
 aac ttt gac gct cat gat tta aac act tta tcc ctt caa ttt cga ata 3088  
 Asn Phe Asp Ala His Asp Leu Asn Thr Leu Ser Leu Gln Phe Arg Ile  
     105              110              115

tta aga caa cat ggt tac aat atc tcc caa a gtaggtccat catttaaaac 3139  
 Leu Arg Gln His Gly Tyr Asn Ile Ser Gln  
 120 125

aattcaccaa aataatacgt tttttctgc atgaaaacta attatcttt gctttattc 3199

gatcatgatc cag aa ttt ttc agc aga ttc caa gat gcg aat ggc aag ttc 3250  
 Lys Phe Ser Arg Phe Gln Asp Ala Asn Gly Lys Phe  
 130 135 140

aag gaa tgt ctt agc aac gac atc agg ggt cta ttg aac tta tac gaa 3298  
 Lys Glu Cys Leu Ser Asn Asp Ile Arg Gly Leu Leu Asn Leu Tyr Glu  
 145 150 155

gct tca cat gta agg act cat gga gaa gat att tta gaa gag gca ctt 3346  
 Ala Ser His Val Arg Thr His Gly Glu Asp Ile Leu Glu Ala Leu  
 160 165 170

gtt ttc tcc act gct cat ctt gag tct gca gct cca cat ttg gag tca 3394  
 Val Phe Ser Thr Ala His Leu Glu Ser Ala Ala Pro His Leu Glu Ser  
 175 180 185

cct ctg agt aag caa gtg act cat gcc ctt gag cag tct ctc cat aag 3442  
 Pro Leu Ser Lys Gln Val Thr His Ala Leu Glu Gln Ser Leu His Lys  
 190 195 200

agc att cca aga gtc gag acg cgc tac ttc atc tcc atc tac gaa gag 3490  
 Ser Ile Pro Arg Val Glu Thr Arg Tyr Phe Ile Ser Ile Tyr Glu Glu  
 205 210 215 220

gag gaa ttt aag aat gat gtg ttg ctt cga ttt gcc aaa ttg gat tac 3538  
 Glu Glu Phe Lys Asn Asp Val Leu Leu Arg Phe Ala Lys Leu Asp Tyr  
 225 230 235

aac tta ctc cag atg ttg cac aaa cac gaa ctt agt gaa gta tca ag 3585  
 Asn Leu Leu Gln Met Leu His Lys His Glu Leu Ser Glu Val Ser Arg  
 240 245 250

gtatacagat gtgttaagtt gaattaaaaa tactagtata aattatttgt tgatagtaat 3645

ttcttaagatt ggtacttatt ttgttag g tgg tgg aaa gat ttg gat ttt gtg 3696  
 Trp Trp Lys Asp Leu Asp Phe Val  
 255 260

aca acg ctt cca tat gct agg gat aga gca gtg gaa tgt tac ttt tgg 3744  
 Thr Thr Leu Pro Tyr Ala Arg Asp Arg Ala Val Glu Cys Tyr Phe Trp  
 265 270 275

acg atg gga gtg tat gct gaa cct caa tac tct cag gct cgt gtc atc 3792  
 Thr Met Gly Val Tyr Ala Glu Pro Gln Tyr Ser Gln Ala Arg Val Ile  
 280 285 290

ctt gca aag act ata gca atg att tcg ata gta gat gac aca ttc gat 3840  
 Leu Ala Lys Thr Ile Ala Met Ile Ser Ile Val Asp Asp Thr Phe Asp  
 295 300 305

gct tat gga ata gta aaa gaa ctt gag gtc tac acc gat gcc ata caa 3888  
 Ala Tyr Gly Ile Val Lys Glu Leu Glu Val Tyr Thr Asp Ala Ile Gln  
 310 315 320

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 Arg  
 325

actaaatctc tttctgtttt attag g tgg gat att agt caa att gat cga ctc 3993  
 Trp Asp Ile Ser Gln Ile Asp Arg Leu  
 330

cca gaa tac atg aaa gtt agt ttt aag gct ctt ttg gat ctc tat gaa 4041  
 Pro Glu Tyr Met Lys Val Ser Phe Lys Ala Leu Leu Asp Leu Tyr Glu  
 335 340 345 350

gat tat gaa aag gag ttg tca aag gat ggc aga tcc gat gtt gtc cac 4089  
 Asp Tyr Glu Lys Glu Leu Ser Lys Asp Gly Arg Ser Asp Val Val His  
 355 360 365

tac gca aaa gaa aga gtaggactca ctgatttcta tttaaaaaca cttgtattta 4144  
 Tyr Ala Lys Glu Arg  
 370

ccttatacta tttctttatt atacaattag atctgttatg ggagtattga tggttgaatg 4204

tcttgtggtt tctgttaaac ag atg aag gag att gtg aga aac tat ttt gta 4256  
 Met Lys Glu Ile Val Arg Asn Tyr Phe Val  
 375 380

gaa gca aag tgg ttc att gag gga tat atg ccg cct gtt tct gag tat 4304  
 Glu Ala Lys Trp Phe Ile Glu Gly Tyr Met Pro Pro Val Ser Glu Tyr  
 385 390 395

ctt agc aat gca tta gct acc agc aca tat tac ttg cta act aca aca 4352  
 Leu Ser Asn Ala Leu Ala Thr Ser Thr Tyr Tyr Leu Leu Thr Thr Thr  
 400 405 410

tcc tat ttg gga gtg aag tca gca aca aag gaa gat ttt gaa tgg ttg 4400  
 Ser Tyr Leu Gly Val Lys Ser Ala Thr Lys Glu Asp Phe Glu Trp Leu  
 415 420 425

gct acg aac cct aaa att ctt gaa gcc aat gtg aca tta tgc cga gtt 4448  
 Ala Thr Asn Pro Lys Ile Leu Glu Ala Asn Val Thr Leu Cys Arg Val  
 430 435 440 445

gtt gat gac ata gca acg tat gag gtaatttagca tcgcattaca ctacataaat 4502  
 Val Asp Asp Ile Ala Thr Tyr Glu  
 450

catcttataa ttttagagttt cagtaattta atacaatttg atttcacata cttataaatg 4562

aattataatt gccattccag gtt gag aag ggt agg ggc caa atc gca aca gga 4615  
 Val Glu Lys Gly Arg Gly Gln Ile Ala Thr Gly  
 455 460

att gag tgt tat atg agg gat tat gac gta tca aca gaa gta gca atg	4663	
Ile Glu Cys Tyr Met Arg Asp Tyr Asp Val Ser Thr Glu Val Ala Met		
465 470 475 480		
gaa aaa ttc caa gag atg gct gag ata gca tgg aag gat gta aat gaa	4711	
Glu Lys Phe Gln Glu Met Ala Glu Ile Ala Trp Lys Asp Val Asn Glu		
485 490 495		
gga att ctt cga cca aca cct gtc tct aca gaa att ctt act cgc att	4759	
Gly Ile Leu Arg Pro Thr Pro Val Ser Thr Glu Ile Leu Thr Arg Ile		
500 505 510		
ctc aat ctt gct cgt att ata gat gtc act tac aag cac aat caa gat	4807	
Leu Asn Leu Ala Arg Ile Ile Asp Val Thr Tyr Lys His Asn Gln Asp		
515 520 525		
gga tac act cat ccc gaa aaa gtt cta aaa cct cac atc att gct tta	4855	
Gly Tyr Thr His Pro Glu Lys Val Leu Lys Pro His Ile Ile Ala Leu		
530 535 540		
ctg gtg gac tcc att gag atc taaaaattta gtaaaattta atttttaaaa	4906	
Leu Val Asp Ser Ile Glu Ile		
545 550		
tgttacgtaa aaaataataa accgtaaaaa taatgaagat taaggcgaac gaaccacgtg	4966	
aggcggaaac gttgagaatg gatgatggaa aatagatgaa tatattgtta tgcataagg	5026	
gtgtttcaca ctcctttgat tttggaaatg catggacatc cgcatgttgc cgactacacc	5086	
tcgaccaatg ttgcgcagaac cacggccgat gcgggcaggc cacggatgac cgttgtgtgc	5146	
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agggcgatgc gggcaggcca cgtccgacgt	5236	
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<213> Solanum tuberosum		
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Met Ala Leu Ala Ile Pro Phe Asn Asn Glu Glu Glu Ile Val Arg Pro		
1 5 10 15		
Val Ala Asn Phe Ser Pro Ser Leu Trp Gly Asp Arg Phe His Ser Phe		
20 25 30		
Ser Leu Asp Asn Gln Val Ala Glu Lys Tyr Ala Gln Glu Ile Glu Thr		
35 40 45		
Leu Lys Glu Gln Thr Arg Ser Leu Leu Ser Ala Ala Ala Cys Gly Ile		
50 55 60		
Thr Leu Ala Glu Lys Leu Asn Leu Ile Asp Ile Val Glu Arg Leu Gly		
65 70 75 80		

Leu Ala Tyr His Phe Glu Lys Gln Ile Asp Asp Met Leu Asp Gln Ile  
 85 90 95

Tyr Lys Ala Asp Pro Asn Phe Asp Ala His Asp Leu Asn Thr Leu Ser  
 100 105 110

Leu Gln Phe Arg Ile Leu Arg Gln His Gly Tyr Asn Ile Ser Gln Lys  
 115 120 125

Phe Phe Ser Arg Phe Gln Asp Ala Asn Gly Lys Phe Lys Glu Cys Leu  
 130 135 140

Ser Asn Asp Ile Arg Gly Leu Leu Asn Leu Tyr Glu Ala Ser His Val  
 145 150 155 160

Arg Thr His Gly Glu Asp Ile Leu Glu Glu Ala Leu Val Phe Ser Thr  
 165 170 175

Ala His Leu Glu Ser Ala Ala Pro His Leu Glu Ser Pro Leu Ser Lys  
 180 185 190

Gln Val Thr His Ala Leu Glu Gln Ser Leu His Lys Ser Ile Pro Arg  
 195 200 205

Val Glu Thr Arg Tyr Phe Ile Ser Ile Tyr Glu Glu Glu Phe Lys  
 210 215 220

Asn Asp Val Leu Leu Arg Phe Ala Lys Leu Asp Tyr Asn Leu Leu Gln  
 225 230 235 240

Met Leu His Lys His Glu Leu Ser Glu Val Ser Arg Trp Trp Lys Asp  
 245 250 255

Leu Asp Phe Val Thr Thr Leu Pro Tyr Ala Arg Asp Arg Ala Val Glu  
 260 265 270

Cys Tyr Phe Trp Thr Met Gly Val Tyr Ala Glu Pro Gln Tyr Ser Gln  
 275 280 285

Ala Arg Val Ile Leu Ala Lys Thr Ile Ala Met Ile Ser Ile Val Asp  
 290 295 300

Asp Thr Phe Asp Ala Tyr Gly Ile Val Lys Glu Leu Glu Val Tyr Thr  
 305 310 315 320

Asp Ala Ile Gln Arg Trp Asp Ile Ser Gln Ile Asp Arg Leu Pro Glu  
 325 330 335

Tyr Met Lys Val Ser Phe Lys Ala Leu Leu Asp Leu Tyr Glu Asp Tyr  
 340 345 350

Glu Lys Glu Leu Ser Lys Asp Gly Arg Ser Asp Val Val His Tyr Ala  
 355 360 365

Lys Glu Arg Met Lys Glu Ile Val Arg Asn Tyr Phe Val Glu Ala Lys  
 370 375 380

Trp Phe Ile Glu Gly Tyr Met Pro Pro Val Ser Glu Tyr Leu Ser Asn  
 385 390 395 400  
 Ala Leu Ala Thr Ser Thr Tyr Tyr Leu Leu Thr Thr Thr Ser Tyr Leu  
 405 410 415  
 Gly Val Lys Ser Ala Thr Lys Glu Asp Phe Glu Trp Leu Ala Thr Asn  
 420 425 430  
 Pro Lys Ile Leu Glu Ala Asn Val Thr Leu Cys Arg Val Val Asp Asp  
 435 440 445  
 Ile Ala Thr Tyr Glu Val Glu Lys Gly Arg Gly Gln Ile Ala Thr Gly  
 450 455 460  
 Ile Glu Cys Tyr Met Arg Asp Tyr Asp Val Ser Thr Glu Val Ala Met  
 465 470 475 480  
 Glu Lys Phe Gln Glu Met Ala Glu Ile Ala Trp Lys Asp Val Asn Glu  
 485 490 495  
 Gly Ile Leu Arg Pro Thr Pro Val Ser Thr Glu Ile Leu Thr Arg Ile  
 500 505 510  
 Leu Asn Leu Ala Arg Ile Ile Asp Val Thr Tyr Lys His Asn Gln Asp  
 515 520 525  
 Gly Tyr Thr His Pro Glu Lys Val Leu Lys Pro His Ile Ile Ala Leu  
 530 535 540  
 Leu Val Asp Ser Ile Glu Ile  
 545 550

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<220>  
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 <222> (5)..(40)

<400> 42  
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 1 5 10

<210> 43  
 <211> 12  
 <212> PRT  
 <213> Solanum tuberosum

<400> 43  
 Met Ala Leu Ala Ile Pro Phe Asn Asn Ala Met Glu  
 1 5 10

&lt;210&gt; 44

&lt;211&gt; 61

&lt;212&gt; DNA

&lt;213&gt; Solanum tuberosum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (5) .. (61)

&lt;400&gt; 44

agaa	atg	gcc	cta	gct	atc	ccc	ttt	aac	aat	gaa	gga	tcc	ccg	ggt	ggt	49
Met	Ala	Leu	Ala	Ile	Pro	Phe	Asn	Asn	Glu	Gly	Ser	Pro	Gly	Gly		
1					5				10						15	

cag	tcc	ctt	atg													61
Gln	Ser	Leu	Met													

&lt;210&gt; 45

&lt;211&gt; 19

&lt;212&gt; PRT

&lt;213&gt; Solanum tuberosum

&lt;400&gt; 45

Met	Ala	Leu	Ala	Ile	Pro	Phe	Asn	Asn	Glu	Gly	Ser	Pro	Gly	Gly	Gln	
1					5				10						15	

Ser	Leu	Met														
-----	-----	-----	--	--	--	--	--	--	--	--	--	--	--	--	--	--

&lt;210&gt; 46

&lt;211&gt; 64

&lt;212&gt; DNA

&lt;213&gt; Solanum tuberosum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (5) .. (64)

&lt;400&gt; 46

agaa	atg	gcc	cta	gct	atc	ccc	ttt	aac	aat	gaa	gag	gaa	tcc	atg	ggt	49
Met	Ala	Leu	Ala	Ile	Pro	Phe	Asn	Asn	Glu	Glu	Glu	Glu	Ser	Met	Gly	
1						5				10					15	

cag	tcc	ctt	atg	tta												64
Gln	Ser	Leu	Met	Leu												
				20												

&lt;210&gt; 47

&lt;211&gt; 20

&lt;212&gt; PRT

&lt;213&gt; Solanum tuberosum

&lt;400&gt; 47

Met Ala Leu Ala Ile Pro Phe Asn Asn Glu Glu Glu Ser Met Gly Gln  
1 5 10 15Ser Leu Met Leu  
20